SFAF • Tuesday, June 5, 2012

Time	Abstract #	Title	Speaker/Sponsor
7:30 - 8:30am		**La Fonda Breakfast Buffet**	**Sponsored by NEB**
8:30 - 8:45		Welcome Intro from Los Alamos National Laboratory	**TBD**
Session I – Chairs: Johar Ali and Donna Muzny			
8:45 - 9:30	FF0032	**Keynote: Towards the Perfect Genome Sequence**	**Dr. George Weinstock**
9:30 – 9:50	FF0119	Building the DOE Systems Biology Knowledgebase	**Tom Brettin**
9:50 - 10:10	FF0106	Genome Sequencing of a Mapping Population Reveals Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen *Phytophthora capsici*	**Joann Mudge**
10:10 – 10:30		**Beverages and Snacks Provided**	**Sponsored by OpGen**
10:30 – 10:50	FF0159	Assembling with Longer Reads and Higher Depths	**Jim Knight**
10:50 – 11:10	FF0122	TBD	**Haley Fiske**
11:10 – 11:30	FF0239	Using the Ion Torrent PGM for de novo Sequencing	**Tim Harkins**
11:30 – 11:50	FF0038	Exploiting Single-Molecule Real-Time DNA Sequencing for Improved Genome Assembly and Methylome Analysis	**Steve Turner**
11:50 - 12:40		**Next Generation Sequencing Technology Panel Discussion**	**Chair - Bob Fulton** **Chair - Patrick Chain**
12:40 – 2:00pm		**Coronado Lunch Buffet**	**Sponsored by illumina**
Session II – Chairs: Alla Lapidus and Bob Fulton			
2:00 – 2:20	FF0060	Ion Torrent Semiconductor Sequencing Allows Rapid, Low Cost Sequencing of the Human Exome	**David Jenkins**

2:20 – 2:40	FF0209	En route to the Clinic: Diagnostic Sequencing Applications Using the Ion Torrent	**Donna Muzny**
2:40 – 2:55	FF0047	Next Generation Sequencing: Possible Application for Forensic DNA Analysis. What does the Person of Interest Look Like?	**Tom Callaghan**
2:55 – 3:10	FF0136	Forensic DNA Standards for Next Generation Sequencing Platforms	**Pete Vallone**
3:10 – 3:40	x	**Beverages and Snacks Provided**	**Sponsored by OpGen**
3:40 - 5:50pm	FF0149	Challenges in Genomic Cloud Computing	**Daniel Bozinov**
	FF0126	NGS for the Masses: Empowering Biologists to Improve Bioinformatic Productivity	**Kashef Qaadri**
	FF0070	The PerkinElmer Omics Laboratory	**Todd Smith**
	FF0111	Genome Assembly and Finishing Using CLC bio Tools	**Marta Matvienko**
	FF0213a	Engineered Polymerases Provide Improved NGS Library Amplification and Enable Novel	**Maryke Appel**
	FF0144	Beyond Basic Target Enrichment: New Tools to fuel your NGS Research	**Jennifer Carter**
	FF0019	Better Computing for Better Bioinformatics	**George Vacek**
	FF0296	RAPID: Ultra High Throughput Sequencing Data Analysis for Quick Microbial Identification	**Robert Yamamoto**
6:00 – 7:30pm	EVEN #s	**Poster Session with Meet & Greet Party (Sponsored by Roche)** **Food & Drinks**	**Sponsored by Roche 6:00pm- 9:00pm**
7:30 - 9:00pm	ODD #s	**Poster Session with Meet & Greet Party (Sponsored by Roche)** **Food & Drinks**	**Sponsored by Roche 6:00pm- 9:00pm**
9:00 - bedtime		**Night on your own - enjoy**	

SFAF • Wednesday, June 6, 2012

Time	Abstract #	Title	Speaker/Sponsor
7:30 - 8:30 am		**Santa Fe Breakfast Buffet**	**Sponsored by NEB**
8:30 - 8:45		Welcome Back	**TBD**
Session III – Chairs: Mike Fitzgerald and Tina Graves			
8:45 - 9:30	FF0043	**Keynote: Plague: A Highly Fit Clonal Pathogen Emerges and Shapes Human History**	**Dr. Paul Keim**
9:30 - 9:50	FF0101	Finishing and Special Motifs: Lessons Learned From CRISPR Analysis Using Next Generation Draft Sequences	**Catherine Campbell**
9:50 - 10:10	FF0160	An Analysis of the Genomic Architecture at Risk Loci for SLE	**Ward Wakeland**
10:10 - 10:30	FF0279	Resolve the Cancer Heterogeneity by Single Cell Sequencing	**Xun Xu**
10:30 - 11:00		**Beverages and Snacks Provided**	**Sponsored by TBD**
11:00 - 11:20	FF0075	Consed and BamView for Next-gen Sequencing	**David Gordon**
11:20 - 11:40	FF0065	Integrating Data from Multiple Human Genome Sequencing Platforms and Bioinformatic Methods to Analyze their Error Profiles and Form Consensus Variant Calls	**Jason Zook**
11:40 - 12:00	FF0088	One Chromosome, One Contig: Hybrid Error Correction and *de novo* Assembly of Single-Molecule Sequencing Reads	**Sergey Koren**
12:00 - 1:20pm		**New Mexican Lunch Buffet**	**Sponsored by Beckman**
Session IV – Chairs: Donna Muzny and Johar Ali			
1:20 - 1:40	FF0108	Recent Advances in High-Throughput, Low-Latency Interfacing for Fast Scanning and Metrology in Genomics Applications	**Scott Jordan**
1:40 - 2:00	FF0186	Pilon Assembly Improvement Software	**Bruce Walker**
2:00 - 2:20	FF0188	Putting the Pieces Together: From Assembly to Analysis	**Sean Sykes**

2:20 - 2:40	**FF0045a**	Finding the Perfect Recipe for de novo Plant Genome Assembly: A Platform Bake-off	**Dan Ader**
2:40 - 3:00	**FF0170**	Finished Prokaryotic Genome Assemblies From a Low-Cost Combination of Short and Long Reads	**Shuangye Yin**
3:00 - 3:20	**FF0211**	Mercury: A Next Generation Sequencing Data Analysis and Annotation Pipeline	**David Sexton**
3:20 - 3:30	**FF0174**	DTRA Algorithm Prize	**Christian Whitchurch**
3:30 - 5:00pm			
		Beverages and Snacks Provided for the Round Table	**Sponsored by TBD**
		Topics TBD: attendees to select from a few choices the week before the meeting	
5:30 - 8:00pm		**Happy Hour at Cowgirl Cafe - Sponsored by LifeTech - Map Will be Provided**	**Sponsored by LifeTech**
8:00 - bedtime		**Dinner and Night on Your Own - Enjoy!!!**	**x**

		SFAF • Thursday, June 7, 2012	
Time	**Abstract #**	**Title**	**Speaker/Sponsor**
7:30 - 8:30am		**Breakfast Buffet**	**Sponsored by NEB**
8:30 - 8:45		Welcome Back	**Chris Detter**
Session V – Chairs: Patrick Chain and Nadia Fedorova			
8:45 - 9:30	FF0042	**Keynote: Environmental Reservoirs of Human Pathogens: The Vibrio cholerae Paradigm**	**Dr. Rita Colwell**
9:30 – 9:50	FF0185	A Rapid Whole Genome Sequencing and Analysis System Supporting Genomic Epidemiology	**Mike FitzGerald**
9:50 – 10:10	FF0173	Endosymbiont Hunting in the Metagenome of Asian Citrus Psyllid (*Diaphorina citri*)	**Surya Saha**
10:10 – 10:30	FF0221	SPAdes: A New Genome Assembly Algorithm and its Applications to Single-Cell Sequencing	**Glenn Tesler**
10:30 – 10:50		**Beverages and Snacks Provided**	**Sponsored by TBD**
10:50 – 11:10	FF0263	Assembly of Large Metagenome Data Sets Using a Convey HC-1 Hybrid-Core Computer	**Alex Copeland**
11:10 – 11:30	FF0034	Metagenomic Assembly: Challenges, Successes, and Validation	**Matt Scholz**
11:30 – 11:50	FF0208	Metagenomics for Etiological Agent Discovery	**Matthew Ross**
11:50 – 12:10	FF0207	Nearly Finished Genomes Produced Using Gel Microdroplet Culturing Reveals Substantial Intraspecies Diversity within the Human Microbiome	**Michael Fitzsimons**
12:10 - 1:30pm		**La Fiesta Plaza Lunch**	**Sponsored by Agilent**
Session VI – Chairs: Mike Fitzgerald and Alla Lapidus			
1:30 - 1:50	FF0006	Rapid Phylogenetic and Functional Classification of Short Genomic	**Ben McMahon**

		Fragments with Signature Peptides	
1:50 - 2:10	FF0229	PanFunPro: Pan-Genome Analysis Based on the Functional Profiles	**Oksana Lukjancenko**
2:10 - 2:30	FF0114	Preparation of Nucleic Acid Libraries for Personalized Sequencing Systems Using an Integrated Microfluidic Hub Technology	**Kamlesh Patel**
2:30 - 2:50	FF0142	Capturing Native Long-Range Contiguity by *in situ* Library Construction and Optical Sequencing	**Jerrod Schwartz**
2:50 - 3:10	FF0256	Fosmid Cre-LoxP Inverse PCR Paired-End (Fosmid CLIP-PE), A Novel Method for Generating Fosmid Pair-End Library	**Ze Peng**
3:10 - 3:30	FF0282	Automated Sequencing Library Preparation and Suppression for Rapid Pathogen Characterization	**Todd Lane**
3:30 - 3:50	FF0109	Evaluation of Multiplexed 16S rRNA Microbial Population Surveys Using llumina MiSeq Platform	**Julien Tremblay**
3:50 - 4:00pm		**Closing Discussions for General Meeting - Discuss Next Year's Meeting**	**Chair - Chris Detter**
Reminder for those interested there is a special Forensic's Session Friday from 8am - noon			